

Amendments to the Specification:

Please replace the title of the invention on page 1 with the following replacement title:

~~Methods of Genetic Analysis of Rat Addressable Oligonucleotide Array of the Rat Genome~~

Please replace the paragraph beginning on page 25 line 4 with the following amended paragraph:

In another embodiment genetic variation may be correlated with variation in gene expression pattern. Much of the genetic variation between individuals is the result of single nucleotide polymorphisms (SNPs). The presence of SNPs in or near a gene may result in differences in gene expression, which may result, for example, from changes in the rate of transcription, the stability of the mRNA, splicing of the mRNA, or translation of the mRNA. In one embodiment an array comprising SEQ ID Nos. ~~1-982,914~~ 1-688,466 and probes to genotype selected SNPs in the ~~mouse~~ rat genome may be used to monitor genotype and expression changes that correlate with differences in genotype.

Please replace the paragraph beginning on page 17 line 20 with the following amended paragraph:

An array is disclosed that allows for simultaneous measurement of relative gene expression levels for at least 20,000 rat genes. Probes of the array are designed to be complementary to 25 contiguous bases of a selected gene. Mismatch probes may be included on the array for use as controls to measure discrimination and specificity. Antisense probes that are derived from the opposite strand of the gene may also be included. Other control sequence probes may also be included. Control probes may be included to assay for manufacturing defects, problems with sample preparation and problems with hybridization. In a preferred embodiment the array is a single solid support so that the expression levels for at least ~~30,000~~ 20,000 ~~mouse~~ rat genes may be simultaneously analyzed in a single experiment using a single hybridization. See, for example the U133 Plus 2.0 Array available from Affymetrix. This array allows analysis of over 47,000 human transcripts on a single chip. In another embodiment the probes are divided so that they are on two or more chips or solid supports. The arrays may also be attached to pegs for high throughput analysis.

Please replace the paragraph beginning on page 19 line 3 with the following amended paragraph:

Each target sequence listed in SEQ ID NOS 1 – 699,466 corresponds to a GenBank database accession number. These accession numbers allow for the identification of sequences located in the GenBank sequence database through the use of computer programs such as BLAST. Access to BLAST is available to the public through the internet at, for example, <http://www.ncbi.nlm.nih.gov> the website hosted by the National Center for Biotechnology Information (NCBI). One of skill in the art will be familiar with the use of the BLAST program to obtain information about particular sequences in order to, for example, determine the GenBank accession number, determine the species from which the sequence is derived, determine the gene from which the sequence is derived, to determine other genes and species which contain similar sequences and to determine the degree of similarity between one sequence and another. All information relating to the target sequences available through the GenBank database is hereby incorporated by reference for all purposes.